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<110> BASF Aktiengesellschaft  
 <120> L-Rhamnose-inducible expression systems  
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gattaa
2046

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&lt;210&gt; 2

&lt;211&gt; 287

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;220&gt;

&lt;221&gt; promoter

&lt;222&gt; (1)..(287)

&lt;223&gt; rhaBAD promoter fragment containing rhaS and rhaR binding sites

&lt;400&gt; 2

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taaattttcg acggaaaacc acgtaaaaaa cgctgatttt tcaagataca gcgtgaattt 120
tcaggaaatg cgggtgagcat cacatcacca caattcagca aattgtgaac atcatcacgt 180
tcatctttcc ctggttgcca atggcccatt ttcctgtcag taacgagaag gtcgcgaatt 240
caggcgcttt ttagactggg cgtaatgaaa ttcagcagga tcacatt
287

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&lt;210&gt; 3

&lt;211&gt; 125

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;220&gt;

&lt;221&gt; promoter

&lt;222&gt; (1)..(125)

&lt;223&gt; rhaBAD promoter fragment containing RhaS binding site

&lt;400&gt; 3

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ttgtgaacat catcacgttc atctttccct gggtgccaat ggcccatttt cctgtcagta 60
acgagaaggt cgcgaaattca ggcgcttttt agactggtcg taatgaaatt cagcaggatc 120
acatt
125

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gcccatatttc ctgtcagtaa cgagaaggtc gcgaattcag gcgcttttta gactggtcgt 120
aat                                             123

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<213> Escherichia coli
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<221> misc_feature
<222> (1)..(51)
<223> palindromic RhaS binding site  of rhaBAD promoter
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<212> DNA
<213> Alcaligenes faecalis
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<223> coding for nitrilase
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Met Gln Thr Arg Lys Ile Val Arg Ala Ala Ala Val Gln Ala Ala Ser
  1             5             10             15

ccc aac tac gat ctg gca acg ggt gtt gat aaa acc att gag ctg gct 96
Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala
          20             25             30

cgt cag gcc cgc gat gag ggc tgt gac ctg atc gtg ttt ggt gaa acc 144
Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr
          35             40             45

tgg ctg ccc gga tat ccc ttc cac gtc tgg ctg ggc gca ccg gcc tgg 192
Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp
          50             55             60

tcg ctg aaa tac agt gcc cgc tac tat gcc aac tcg ctc tcg ctg gac 240
Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp
          65             70             75             80

agt gca gag ttt caa cgc att gcc cag gcc gca cgg acc ttg ggt att 288
Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile
          85             90             95

ttc atc gca ctg ggt tat agc gag cgc agc ggc ggc agc ctt tac ctg 336
Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu
          100             105             110

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ggc	caa	tgc	ctg	atc	gac	gac	aag	ggc	gag	atg	ctg	tgg	tcg	cgt	cgc	384
Gly	Gln	Cys	Leu	Ile	Asp	Asp	Lys	Gly	Glu	Met	Leu	Trp	Ser	Arg	Arg	
		115					120					125				
aaa	ctc	aaa	ccc	acg	cat	gta	gag	cgc	acc	gta	ttt	ggt	gaa	ggt	tat	432
Lys	Leu	Lys	Pro	Thr	His	Val	Glu	Arg	Thr	Val	Phe	Gly	Glu	Gly	Tyr	
		130				135					140					
gcc	cgt	gat	ctg	att	gtg	tcc	gac	aca	gaa	ctg	gga	cgc	gtc	ggt	gct	480
Ala	Arg	Asp	Leu	Ile	Val	Ser	Asp	Thr	Glu	Leu	Gly	Arg	Val	Gly	Ala	
					150					155					160	
cta	tgc	tgc	tgg	gag	cat	ttg	tcg	ccc	ttg	agc	aag	tac	gcg	ctg	tac	528
Leu	Cys	Cys	Trp	Glu	His	Leu	Ser	Pro	Leu	Ser	Lys	Tyr	Ala	Leu	Tyr	
				165					170					175		
tcc	cag	cat	gaa	gcc	att	cac	att	gct	gcc	tgg	ccg	tcg	ttt	tcg	cta	576
Ser	Gln	His	Glu	Ala	Ile	His	Ile	Ala	Ala	Trp	Pro	Ser	Phe	Ser	Leu	
			180					185					190			
tac	agc	gaa	cag	gcc	cac	gcc	ctc	agt	gcc	aag	gtg	aac	atg	gct	gcc	624
Tyr	Ser	Glu	Gln	Ala	His	Ala	Leu	Ser	Ala	Lys	Val	Asn	Met	Ala	Ala	
		195					200					205				
tcg	caa	atc	tat	tcg	gtt	gaa	ggc	cag	tgc	ttt	acc	atc	gcc	gcc	agc	672
Ser	Gln	Ile	Tyr	Ser	Val	Glu	Gly	Gln	Cys	Phe	Thr	Ile	Ala	Ala	Ser	
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agt	gtg	gtc	acc	caa	gag	acg	cta	gac	atg	ctg	gaa	gtg	ggt	gaa	cac	720
Ser	Val	Val	Thr	Gln	Glu	Thr	Leu	Asp	Met	Leu	Glu	Val	Gly	Glu	His	
					230					235					240	
aac	gcc	ccc	ttg	ctg	aaa	gtg	ggc	ggc	ggc	agt	tcc	atg	att	ttt	gcg	768
Asn	Ala	Pro	Leu	Leu	Lys	Val	Gly	Gly	Gly	Ser	Ser	Met	Ile	Phe	Ala	
				245				250						255		
ccg	gac	gga	cgc	aca	ctg	gct	ccc	tac	ctg	cct	cac	gat	gcc	gag	ggc	816
Pro	Asp	Gly	Arg	Thr	Leu	Ala	Pro	Tyr	Leu	Pro	His	Asp	Ala	Glu	Gly	
			260					265					270			
ttg	atc	att	gcc	gat	ctg	aat	atg	gag	gag	att	gcc	ttc	gcc	aaa	gcg	864
Leu	Ile	Ile	Ala	Asp	Leu	Asn	Met	Glu	Glu	Ile	Ala	Phe	Ala	Lys	Ala	
		275					280					285				
atc	aat	gac	ccc	gta	ggc	cac	tat	tcc	aaa	ccc	gag	gcc	acc	cgt	ctg	912
Ile	Asn	Asp	Pro	Val	Gly	His	Tyr	Ser	Lys	Pro	Glu	Ala	Thr	Arg	Leu	
		290				295					300					
gtg	ctg	gac	ttg	ggg	cac	cga	gac	ccc	atg	act	cgg	gtg	cac	tcc	aaa	960
Val	Leu	Asp	Leu	Gly	His	Arg	Asp	Pro	Met	Thr	Arg	Val	His	Ser	Lys	
					310					315					320	
agc	gtg	acc	agg	gaa	gag	gct	ccc	gag	caa	ggt	gtg	caa	agc	aag	att	1008
Ser	Val	Thr	Arg	Glu	Glu	Ala	Pro	Glu	Gln	Gly	Val	Gln	Ser	Lys	Ile	
				325					330					335		
gcc	tca	gtc	gct	atc	agc	cat	cca	cag	gac	tcg	gac	aca	ctg	cta	gtg	1056
Ala	Ser	Val	Ala	Ile	Ser	His	Pro	Gln	Asp	Ser	Asp	Thr	Leu	Leu	Val	
			340					345					350			
caa	gag	ccg	tct	tga												1071
Gln	Glu	Pro	Ser													
			355													

&lt;210&gt; 7

&lt;211&gt; 356

&lt;212&gt; PRT

<213> *Alcaligenes faecalis*

&lt;400&gt; .7

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Pro	Asn	Tyr	Asp	Leu	Ala	Thr	Gly	Val	Asp	Lys	Thr	Ile	Glu	Leu	Ala	20	25	30	
Arg	Gln	Ala	Arg	Asp	Glu	Gly	Cys	Asp	Leu	Ile	Val	Phe	Gly	Glu	Thr	35	40	45	
Trp	Leu	Pro	Gly	Tyr	Pro	Phe	His	Val	Trp	Leu	Gly	Ala	Pro	Ala	Trp	50	55	60	
Ser	Leu	Lys	Tyr	Ser	Ala	Arg	Tyr	Tyr	Ala	Asn	Ser	Leu	Ser	Leu	Asp	65	70	75	80
Ser	Ala	Glu	Phe	Gln	Arg	Ile	Ala	Gln	Ala	Ala	Arg	Thr	Leu	Gly	Ile	85	90	95	
Phe	Ile	Ala	Leu	Gly	Tyr	Ser	Glu	Arg	Ser	Gly	Gly	Ser	Leu	Tyr	Leu	100	105	110	
Gly	Gln	Cys	Leu	Ile	Asp	Asp	Lys	Gly	Glu	Met	Leu	Trp	Ser	Arg	Arg	115	120	125	
Lys	Leu	Lys	Pro	Thr	His	Val	Glu	Arg	Thr	Val	Phe	Gly	Glu	Gly	Tyr	130	135	140	
Ala	Arg	Asp	Leu	Ile	Val	Ser	Asp	Thr	Glu	Leu	Gly	Arg	Val	Gly	Ala	145	150	155	160
Leu	Cys	Cys	Trp	Glu	His	Leu	Ser	Pro	Leu	Ser	Lys	Tyr	Ala	Leu	Tyr	165	170	175	
Ser	Gln	His	Glu	Ala	Ile	His	Ile	Ala	Ala	Trp	Pro	Ser	Phe	Ser	Leu	180	185	190	
Tyr	Ser	Glu	Gln	Ala	His	Ala	Leu	Ser	Ala	Lys	Val	Asn	Met	Ala	Ala	195	200	205	
Ser	Gln	Ile	Tyr	Ser	Val	Glu	Gly	Gln	Cys	Phe	Thr	Ile	Ala	Ala	Ser	210	215	220	
Ser	Val	Val	Thr	Gln	Glu	Thr	Leu	Asp	Met	Leu	Glu	Val	Gly	Glu	His	225	230	235	240
Asn	Ala	Pro	Leu	Leu	Lys	Val	Gly	Gly	Gly	Ser	Ser	Met	Ile	Phe	Ala	245	250	255	
Pro	Asp	Gly	Arg	Thr	Leu	Ala	Pro	Tyr	Leu	Pro	His	Asp	Ala	Glu	Gly	260	265	270	
Leu	Ile	Ile	Ala	Asp	Leu	Asn	Met	Glu	Glu	Ile	Ala	Phe	Ala	Lys	Ala	275	280	285	
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Val	Leu	Asp	Leu	Gly	His	Arg	Asp	Pro	Met	Thr	Arg	Val	His	Ser	Lys	305	310	315	320
Ser	Val	Thr	Arg	Glu	Glu	Ala	Pro	Glu	Gln	Gly	Val	Gln	Ser	Lys	Ile	325	330	335	
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Gln Glu Pro Ser  
355

<210> 8

<211> 1260

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(1257)

<223> coding for rhaA (L-rhamnose isomerase)

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gcg gcg gtg ggg att gat gtc gag gag gcg ctg cgc caa ctt gat cgt	96
Ala Ala Val Gly Ile Asp Val Glu Glu Ala Leu Arg Gln Leu Asp Arg	
20 25 30	
tta ccc gtt tca atg cac tgc tgg cag ggc gat gat gtt tcc ggt ttt	144
Leu Pro Val Ser Met His Cys Trp Gln Gly Asp Asp Val Ser Gly Phe	
35 40 45	
gaa aac ccg gaa ggt tcg ctg acc ggg ggg att cag gcc aca ggc aat	192
Glu Asn Pro Glu Gly Ser Leu Thr Gly Gly Ile Gln Ala Thr Gly Asn	
50 55 60	
tat ccg ggc aaa gcg cgt aat gcc agt gag cta cgt gcc gat ctg gaa	240
Tyr Pro Gly Lys Ala Arg Asn Ala Ser Glu Leu Arg Ala Asp Leu Glu	
65 70 75 80	
cag gct atg cgg ctg att ccg ggg ccg aaa cgg ctt aat tta cat gcc	288
Gln Ala Met Arg Leu Ile Pro Gly Pro Lys Arg Leu Asn Leu His Ala	
85 90 95	
atc tat ctg gaa tca gat acg cca gtc tcg cgc gac cag atc aaa cca	336
Ile Tyr Leu Glu Ser Asp Thr Pro Val Ser Arg Asp Gln Ile Lys Pro	
100 105 110	
gag cac ttc aaa aac tgg gtt gaa tgg gcg aaa gcc aat cag ctc ggt	384
Glu His Phe Lys Asn Trp Val Glu Trp Ala Lys Ala Asn Gln Leu Gly	
115 120 125	
ctg gat ttt aac ccc tcc tgc ttt tcg cat ccg cta agc gcc gat ggc	432
Leu Asp Phe Asn Pro Ser Cys Phe Ser His Pro Leu Ser Ala Asp Gly	
130 135 140	
ttt acg ctt tcc cat gcc gac gac agc att cgc cag ttc tgg att gat	480
Phe Thr Leu Ser His Ala Asp Asp Ser Ile Arg Gln Phe Trp Ile Asp	
145 150 155 160	
cac tgc aaa gcc agc cgt cgc gtt tcg gcc tat ttt ggc gag caa ctc	528
His Cys Lys Ala Ser Arg Arg Val Ser Ala Tyr Phe Gly Glu Gln Leu	
165 170 175	
ggc aca cca tcg gtg atg aac atc tgg atc ccg gat ggt atg aaa gat	576
Gly Thr Pro Ser Val Met Asn Ile Trp Ile Pro Asp Gly Met Lys Asp	
180 185 190	
atc acc gtt gac cgt ctc gcc ccg cgt cag cgt ctg ctg gca gca ctg	624
Ile Thr Val Asp Arg Leu Ala Pro Arg Gln Arg Leu Leu Ala Ala Leu	
195 200 205	

7

gat gag gtg atc agc gag aag cta aac cct gcg cac cat atc gac gcc	672
Asp Glu Val Ile Ser Glu Lys Leu Asn Pro Ala His His Ile Asp Ala	
210 215 220	
gtt gag agc aaa ttg ttt ggc att ggc gca gag agc tac acg gtt ggc	720
Val Glu Ser Lys Leu Phe Gly Ile Gly Ala Glu Ser Tyr Thr Val Gly	
225 230 235 240	
tcc aat gag ttt tac atg ggg tat gcc acc agc cgc cag act gcg ctg	768
Ser Asn Glu Phe Tyr Met Gly Tyr Ala Thr Ser Arg Gln Thr Ala Leu	
245 250 255	
tgc ctg gac gcc ggg cac ttc cac ccg act gaa gtg att tcc gac aag	816
Cys Leu Asp Ala Gly His Phe His Pro Thr Glu Val Ile Ser Asp Lys	
260 265 270	
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Ile Ser Ala Ala Met Leu Tyr Val Pro Gln Leu Leu Leu His Val Ser	
275 280 285	
cgt ccg gtt cgc tgg gac agc gat cac gta gtg ctg ctg gat gat gaa	912
Arg Pro Val Arg Trp Asp Ser Asp His Val Val Leu Leu Asp Asp Glu	
290 295 300	
acc cag gca att gcc agt gag att gtg cgt cac gat ctg ttt gac cgg	960
Thr Gln Ala Ile Ala Ser Glu Ile Val Arg His Asp Leu Phe Asp Arg	
305 310 315 320	
gtg cat atc ggc ctt gac ttc ttc gat gcc tct atc aac cgc att gcc	1008
Val His Ile Gly Leu Asp Phe Phe Asp Ala Ser Ile Asn Arg Ile Ala	
325 330 335	
gcg tgg gtc att ggt aca cgc aat atg aaa aaa gcc ctg ctg cgt gcg	1056
Ala Trp Val Ile Gly Thr Arg Asn Met Lys Lys Ala Leu Leu Arg Ala	
340 345 350	
ttg ctg gaa cct acc gct gac gtg cgc aag ctg gaa gcg gcg ggc gat	1104
Leu Leu Glu Pro Thr Ala Asp Val Arg Lys Leu Glu Ala Ala Gly Asp	
355 360 365	
tac act gcg cgt ctg gca ctg ctg gaa gag cag aaa tcg ttg ccg tgg	1152
Tyr Thr Ala Arg Leu Ala Leu Leu Glu Glu Gln Lys Ser Leu Pro Trp	
370 375 380	
cag gcg gtc tgg gaa atg tat tgc caa cgt cac gat acg cca gca ggt	1200
Gln Ala Val Trp Glu Met Tyr Cys Gln Arg His Asp Thr Pro Ala Gly	
385 390 395 400	
agc gaa tgg ctg gag agc gtg cgg gct tat gag aaa gaa att ttg agt	1248
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cgc cgc ggg taa	1260
Arg Arg Gly	
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20 25 30	

Leu	Pro	Val	Ser	Met	His	Cys	Trp	Gln	Gly	Asp	Asp	Val	Ser	Gly	Phe	35	40	45
Glu	Asn	Pro	Glu	Gly	Ser	Leu	Thr	Gly	Gly	Ile	Gln	Ala	Thr	Gly	Asn	50	55	60
Tyr	Pro	Gly	Lys	Ala	Arg	Asn	Ala	Ser	Glu	Leu	Arg	Ala	Asp	Leu	Glu	65	70	75
Gln	Ala	Met	Arg	Leu	Ile	Pro	Gly	Pro	Lys	Arg	Leu	Asn	Leu	His	Ala	85	90	95
Ile	Tyr	Leu	Glu	Ser	Asp	Thr	Pro	Val	Ser	Arg	Asp	Gln	Ile	Lys	Pro	100	105	110
Glu	His	Phe	Lys	Asn	Trp	Val	Glu	Trp	Ala	Lys	Ala	Asn	Gln	Leu	Gly	115	120	125
Leu	Asp	Phe	Asn	Pro	Ser	Cys	Phe	Ser	His	Pro	Leu	Ser	Ala	Asp	Gly	130	135	140
Phe	Thr	Leu	Ser	His	Ala	Asp	Asp	Ser	Ile	Arg	Gln	Phe	Trp	Ile	Asp	145	150	155
His	Cys	Lys	Ala	Ser	Arg	Arg	Val	Ser	Ala	Tyr	Phe	Gly	Glu	Gln	Leu	165	170	175
Gly	Thr	Pro	Ser	Val	Met	Asn	Ile	Trp	Ile	Pro	Asp	Gly	Met	Lys	Asp	180	185	190
Ile	Thr	Val	Asp	Arg	Leu	Ala	Pro	Arg	Gln	Arg	Leu	Leu	Ala	Ala	Leu	195	200	205
Asp	Glu	Val	Ile	Ser	Glu	Lys	Leu	Asn	Pro	Ala	His	His	Ile	Asp	Ala	210	215	220
Val	Glu	Ser	Lys	Leu	Phe	Gly	Ile	Gly	Ala	Glu	Ser	Tyr	Thr	Val	Gly	225	230	235
Ser	Asn	Glu	Phe	Tyr	Met	Gly	Tyr	Ala	Thr	Ser	Arg	Gln	Thr	Ala	Leu	245	250	255
Cys	Leu	Asp	Ala	Gly	His	Phe	His	Pro	Thr	Glu	Val	Ile	Ser	Asp	Lys	260	265	270
Ile	Ser	Ala	Ala	Met	Leu	Tyr	Val	Pro	Gln	Leu	Leu	Leu	His	Val	Ser	275	280	285
Arg	Pro	Val	Arg	Trp	Asp	Ser	Asp	His	Val	Val	Leu	Leu	Asp	Asp	Glu	290	295	300
Thr	Gln	Ala	Ile	Ala	Ser	Glu	Ile	Val	Arg	His	Asp	Leu	Phe	Asp	Arg	305	310	315
Val	His	Ile	Gly	Leu	Asp	Phe	Phe	Asp	Ala	Ser	Ile	Asn	Arg	Ile	Ala	325	330	335
Ala	Trp	Val	Ile	Gly	Thr	Arg	Asn	Met	Lys	Lys	Ala	Leu	Leu	Arg	Ala	340	345	350
Leu	Leu	Glu	Pro	Thr	Ala	Asp	Val	Arg	Lys	Leu	Glu	Ala	Ala	Gly	Asp	355	360	365
Tyr	Thr	Ala	Arg	Leu	Ala	Leu	Leu	Glu	Glu	Gln	Lys	Ser	Leu	Pro	Trp	370	375	380
Gln	Ala	Val	Trp	Glu	Met	Tyr	Cys	Gln	Arg	His	Asp	Thr	Pro	Ala	Gly	385	390	395
Ser	Glu	Trp	Leu	Glu	Ser	Val	Arg	Ala	Tyr	Glu	Lys	Glu	Ile	Leu	Ser	405	410	415



Arg Arg Gly

&lt;210&gt; 10

&lt;211&gt; 1470

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1467)

&lt;223&gt; coding for rhaB (rhamnulokinase)

&lt;400&gt; 10

atg acc ttt cgc aat tgt gtc gcc gtc gat ctc ggc gca tcc agt ggg	48
Met Thr Phe Arg Asn Cys Val Ala Val Asp Leu Gly Ala Ser Ser Gly	
1 5 10 15	
cgc gtg atg ctg gcg cgt tac gag cgt gaa tgc cgc agc ctg acg ctg	96
Arg Val Met Leu Ala Arg Tyr Glu Arg Glu Cys Arg Ser Leu Thr Leu	
20 25 30	
cgc gaa atc cat cgt ttt aac aat ggg ctg cat agt cag aac ggc tat	144
Arg Glu Ile His Arg Phe Asn Asn Gly Leu His Ser Gln Asn Gly Tyr	
35 40 45	
gtc acc tgg gat gtg gat agc ctt gaa agt gcc att cgc ctt gga tta	192
Val Thr Trp Asp Val Asp Ser Leu Glu Ser Ala Ile Arg Leu Gly Leu	
50 55 60	
aac aag gtg tgc gag gaa ggg att cgt atc gat agc att ggg att gat	240
Asn Lys Val Cys Glu Glu Gly Ile Arg Ile Asp Ser Ile Gly Ile Asp	
65 70 75 80	
acc tgg ggc gtg gac ttt gtg ctg ctc gac caa cag ggt cag cgt gtg	288
Thr Trp Gly Val Asp Phe Val Leu Leu Asp Gln Gln Gly Gln Arg Val	
85 90 95	
ggc ctg ccc gtt gct tat cgc gat agc cgc acc aat ggc cta atg gcg	336
Gly Leu Pro Val Ala Tyr Arg Asp Ser Arg Thr Asn Gly Leu Met Ala	
100 105 110	
cag gca caa caa caa ctc ggc aaa cgc gat att tat caa cgt agc ggc	384
Gln Ala Gln Gln Gln Leu Gly Lys Arg Asp Ile Tyr Gln Arg Ser Gly	
115 120 125	
atc cag ttt ctg ccc ttc aat acg ctt tat cag ttg cgt gcg ctg acg	432
Ile Gln Phe Leu Pro Phe Asn Thr Leu Tyr Gln Leu Arg Ala Leu Thr	
130 135 140	
gag caa caa cct gaa ctt att cca cac att gct cac gct ctg ctg atg	480
Glu Gln Gln Pro Glu Leu Ile Pro His Ile Ala His Ala Leu Leu Met	
145 150 155 160	
ccg gat tac ttc agt tat cgc ctg acc ggc aag atg aac tgg gaa tat	528
Pro Asp Tyr Phe Ser Tyr Arg Leu Thr Gly Lys Met Asn Trp Glu Tyr	
165 170 175	
acc aac gcc acg acc acg caa ctg gtc aat atc aat agc gac gac tgg	576
Thr Asn Ala Thr Thr Thr Gln Leu Val Asn Ile Asn Ser Asp Asp Trp	
180 185 190	
gac gag tcg cta ctg gcg tgg agc ggg gcc aac aaa gcc tgg ttt ggt	624
Asp Glu Ser Leu Leu Ala Trp Ser Gly Ala Asn Lys Ala Trp Phe Gly	
195 200 205	

## 10

cgc	ccg	acg	cat	ccg	ggt	aat	gtc	ata	ggt	cac	tgg	att	tgc	ccg	cag	672
Arg	Pro	Thr	His	Pro	Gly	Asn	Val	Ile	Gly	His	Trp	Ile	Cys	Pro	Gln	
	210					215					220					
ggt	aat	gag	att	cca	gtg	gtc	gcc	gtt	gcc	agc	cat	gat	acc	gcc	agc	720
Gly	Asn	Glu	Ile	Pro	Val	Val	Ala	Val	Ala	Ser	His	Asp	Thr	Ala	Ser	
225					230					235					240	
gcg	gtt	atc	gcc	tcg	ccg	tta	aac	ggc	tca	cgt	gct	gct	tat	ctc	tct	768
Ala	Val	Ile	Ala	Ser	Pro	Leu	Asn	Gly	Ser	Arg	Ala	Ala	Tyr	Leu	Ser	
				245					250					255		
tct	ggc	acc	tgg	tca	ttg	atg	ggc	ttc	gaa	agc	cag	acg	cca	ttt	acc	816
Ser	Gly	Thr	Trp	Ser	Leu	Met	Gly	Phe	Glu	Ser	Gln	Thr	Pro	Phe	Thr	
			260					265					270			
aat	gac	acg	gca	ctg	gca	gcc	aac	atc	acc	aat	gaa	ggc	ggg	gcg	gaa	864
Asn	Asp	Thr	Ala	Leu	Ala	Ala	Asn	Ile	Thr	Asn	Glu	Gly	Gly	Ala	Glu	
		275					280					285				
ggt	cgc	tat	cgg	gtg	ctg	aaa	aat	att	atg	ggc	tta	tgg	ctg	ctt	cag	912
Gly	Arg	Tyr	Arg	Val	Leu	Lys	Asn	Ile	Met	Gly	Leu	Trp	Leu	Leu	Gln	
	290					295					300					
cga	gtg	ctt	cag	gag	cag	caa	atc	aac	gat	ctt	ccg	gcg	ctt	atc	tcc	960
Arg	Val	Leu	Gln	Glu	Gln	Gln	Ile	Asn	Asp	Leu	Pro	Ala	Leu	Ile	Ser	
305					310					315					320	
gcg	aca	cag	gca	ctt	ccg	gct	tgc	cgc	ttc	att	atc	aat	ccc	aat	gac	1008
Ala	Thr	Gln	Ala	Leu	Pro	Ala	Cys	Arg	Phe	Ile	Ile	Asn	Pro	Asn	Asp	
				325					330					335		
gat	cgc	ttt	att	aat	cct	gag	acg	atg	tgc	agc	gaa	att	cag	gct	gcg	1056
Asp	Arg	Phe	Ile	Asn	Pro	Glu	Thr	Met	Cys	Ser	Glu	Ile	Gln	Ala	Ala	
			340					345					350			
tgt	cgg	gaa	acg	gcg	caa	ccg	atc	ccg	gaa	agt	gat	gct	gaa	ctg	gcg	1104
Cys	Arg	Glu	Thr	Ala	Gln	Pro	Ile	Pro	Glu	Ser	Asp	Ala	Glu	Leu	Ala	
		355					360					365				
cgc	tgc	att	ttc	gac	agt	ctg	gcg	ctg	ctg	tat	gcc	gat	gtg	ttg	cat	1152
Arg	Cys	Ile	Phe	Asp	Ser	Leu	Ala	Leu	Leu	Tyr	Ala	Asp	Val	Leu	His	
	370					375					380					
gag	ctg	gcg	cag	ctg	cgc	ggt	gaa	gat	ttc	tcg	caa	ctg	cat	att	gtc	1200
Glu	Leu	Ala	Gln	Leu	Arg	Gly	Glu	Asp	Phe	Ser	Gln	Leu	His	Ile	Val	
385					390					395					400	
ggc	gga	ggc	tgc	cag	aac	acg	ctg	ctc	aac	cag	cta	tgc	gcc	gat	gcc	1248
Gly	Gly	Gly	Cys	Gln	Asn	Thr	Leu	Leu	Asn	Gln	Leu	Cys	Ala	Asp	Ala	
				405					410					415		
tgc	ggt	att	cgg	gtg	atc	gcc	ggg	cct	gtt	gaa	gcc	tcg	acg	ctc	ggc	1296
Cys	Gly	Ile	Arg	Val	Ile	Ala	Gly	Pro	Val	Glu	Ala	Ser	Thr	Leu	Gly	
			420					425					430			
aat	atc	ggc	atc	cag	tta	atg	acg	ctg	gat	gaa	ctc	aac	aat	gtg	gat	1344
Asn	Ile	Gly	Ile	Gln	Leu	Met	Thr	Leu	Asp	Glu	Leu	Asn	Asn	Val	Asp	
		435					440					445				
gat	ttc	cgt	cag	gtc	gtc	agc	acc	acc	gcg	aat	ctg	acc	acc	ttt	acc	1392
Asp	Phe	Arg	Gln	Val	Val	Ser	Thr	Thr	Ala	Asn	Leu	Thr	Thr	Phe	Thr	
	450					455					460					
cct	aat	cct	gac	agt	gaa	att	gcc	cac	tat	gtg	gcg	cag	att	cac	tct	1440
Pro	Asn	Pro	Asp	Ser	Glu	Ile	Ala	His	Tyr	Val	Ala	Gln	Ile	His	Ser	
465					470					475					480	

aca cga cag aca aag gag ctt tgc gca tga  
 Thr Arg Gln Thr Lys Glu Leu Cys Ala  
 485

1470

&lt;210&gt; 11

&lt;211&gt; 489

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 11

Met	Thr	Phe	Arg	Asn	Cys	Val	Ala	Val	Asp	Leu	Gly	Ala	Ser	Ser	Gly
1				5					10					15	
Arg	Val	Met	Leu	Ala	Arg	Tyr	Glu	Arg	Glu	Cys	Arg	Ser	Leu	Thr	Leu
			20					25					30		
Arg	Glu	Ile	His	Arg	Phe	Asn	Asn	Gly	Leu	His	Ser	Gln	Asn	Gly	Tyr
		35					40					45			
Val	Thr	Trp	Asp	Val	Asp	Ser	Leu	Glu	Ser	Ala	Ile	Arg	Leu	Gly	Leu
	50					55					60				
Asn	Lys	Val	Cys	Glu	Glu	Gly	Ile	Arg	Ile	Asp	Ser	Ile	Gly	Ile	Asp
65					70					75					80
Thr	Trp	Gly	Val	Asp	Phe	Val	Leu	Leu	Asp	Gln	Gln	Gly	Gln	Arg	Val
				85					90					95	
Gly	Leu	Pro	Val	Ala	Tyr	Arg	Asp	Ser	Arg	Thr	Asn	Gly	Leu	Met	Ala
			100					105					110		
Gln	Ala	Gln	Gln	Gln	Leu	Gly	Lys	Arg	Asp	Ile	Tyr	Gln	Arg	Ser	Gly
		115					120					125			
Ile	Gln	Phe	Leu	Pro	Phe	Asn	Thr	Leu	Tyr	Gln	Leu	Arg	Ala	Leu	Thr
	130					135					140				
Glu	Gln	Gln	Pro	Glu	Leu	Ile	Pro	His	Ile	Ala	His	Ala	Leu	Leu	Met
145					150					155					160
Pro	Asp	Tyr	Phe	Ser	Tyr	Arg	Leu	Thr	Gly	Lys	Met	Asn	Trp	Glu	Tyr
				165					170					175	
Thr	Asn	Ala	Thr	Thr	Thr	Gln	Leu	Val	Asn	Ile	Asn	Ser	Asp	Asp	Trp
			180					185					190		
Asp	Glu	Ser	Leu	Leu	Ala	Trp	Ser	Gly	Ala	Asn	Lys	Ala	Trp	Phe	Gly
		195				200						205			
Arg	Pro	Thr	His	Pro	Gly	Asn	Val	Ile	Gly	His	Trp	Ile	Cys	Pro	Gln
	210					215					220				
Gly	Asn	Glu	Ile	Pro	Val	Val	Ala	Val	Ala	Ser	His	Asp	Thr	Ala	Ser
225					230					235					240
Ala	Val	Ile	Ala	Ser	Pro	Leu	Asn	Gly	Ser	Arg	Ala	Ala	Tyr	Leu	Ser
				245					250					255	
Ser	Gly	Thr	Trp	Ser	Leu	Met	Gly	Phe	Glu	Ser	Gln	Thr	Pro	Phe	Thr
			260					265					270		
Asn	Asp	Thr	Ala	Leu	Ala	Ala	Asn	Ile	Thr	Asn	Glu	Gly	Gly	Ala	Glu
		275					280					285			
Gly	Arg	Tyr	Arg	Val	Leu	Lys	Asn	Ile	Met	Gly	Leu	Trp	Leu	Leu	Gln
	290					295					300				
Arg	Val	Leu	Gln	Glu	Gln	Gln	Ile	Asn	Asp	Leu	Pro	Ala	Leu	Ile	Ser
305					310					315					320

## 12

Ala	Thr	Gln	Ala	Leu	Pro	Ala	Cys	Arg	Phe	Ile	Ile	Asn	Pro	Asn	Asp	
				325					330					335		
Asp	Arg	Phe	Ile	Asn	Pro	Glu	Thr	Met	Cys	Ser	Glu	Ile	Gln	Ala	Ala	
			340					345					350			
Cys	Arg	Glu	Thr	Ala	Gln	Pro	Ile	Pro	Glu	Ser	Asp	Ala	Glu	Leu	Ala	
		355					360					365				
Arg	Cys	Ile	Phe	Asp	Ser	Leu	Ala	Leu	Leu	Tyr	Ala	Asp	Val	Leu	His	
	370					375					380					
Glu	Leu	Ala	Gln	Leu	Arg	Gly	Glu	Asp	Phe	Ser	Gln	Leu	His	Ile	Val	
385					390					395					400	
Gly	Gly	Gly	Cys	Gln	Asn	Thr	Leu	Leu	Asn	Gln	Leu	Cys	Ala	Asp	Ala	
			405						410					415		
Cys	Gly	Ile	Arg	Val	Ile	Ala	Gly	Pro	Val	Glu	Ala	Ser	Thr	Leu	Gly	
			420					425					430			
Asn	Ile	Gly	Ile	Gln	Leu	Met	Thr	Leu	Asp	Glu	Leu	Asn	Asn	Val	Asp	
		435					440					445				
Asp	Phe	Arg	Gln	Val	Val	Ser	Thr	Thr	Ala	Asn	Leu	Thr	Thr	Phe	Thr	
	450					455					460					
Pro	Asn	Pro	Asp	Ser	Glu	Ile	Ala	His	Tyr	Val	Ala	Gln	Ile	His	Ser	
465					470					475					480	
Thr	Arg	Gln	Thr	Lys	Glu	Leu	Cys	Ala								
				485												

&lt;210&gt; 12

&lt;211&gt; 825

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(822)

&lt;223&gt; coding for rhaD (rhamnulose-phosphate aldolase)

&lt;400&gt; 12

atg	caa	aac	att	act	cag	tcc	tgg	ttt	gtc	cag	gga	atg	atc	aaa	gcc	48
Met	Gln	Asn	Ile	Thr	Gln	Ser	Trp	Phe	Val	Gln	Gly	Met	Ile	Lys	Ala	
1				5					10					15		
acc	acc	gac	gcc	tgg	ctg	aaa	ggc	tgg	gat	gag	cgc	aac	ggc	ggc	aac	96
Thr	Thr	Asp	Ala	Trp	Leu	Lys	Gly	Trp	Asp	Glu	Arg	Asn	Gly	Gly	Asn	
			20					25					30			
ctg	acg	cta	cgc	ctg	gat	gac	gcc	gat	atc	gca	cca	tat	cac	gac	aat	144
Leu	Thr	Leu	Arg	Leu	Asp	Asp	Ala	Asp	Ile	Ala	Pro	Tyr	His	Asp	Asn	
			35				40					45				
ttc	cac	caa	caa	ccg	cgc	tat	atc	ccg	ctc	agc	cag	ccc	atg	cct	tta	192
Phe	His	Gln	Gln	Pro	Arg	Tyr	Ile	Pro	Leu	Ser	Gln	Pro	Met	Pro	Leu	
	50					55					60					
ctg	gca	aat	aca	ccg	ttt	att	gtc	acc	ggc	tcg	ggc	aaa	ttc	ttc	cgt	240
Leu	Ala	Asn	Thr	Pro	Phe	Ile	Val	Thr	Gly	Ser	Gly	Lys	Phe	Phe	Arg	
65					70				75						80	
aac	gtc	cag	ctt	gat	cct	gcg	gct	aac	tta	ggc	atc	gta	aaa	gtc	gac	288
Asn	Val	Gln	Leu	Asp	Pro	Ala	Ala	Asn	Leu	Gly	Ile	Val	Lys	Val	Asp	
				85					90					95		

## 13

agc gac ggc gcg ggc tac cac att ctt tgg ggg tta acc aac gaa gcc 336  
 Ser Asp Gly Ala Gly Tyr His Ile Leu Trp Gly Leu Thr Asn Glu Ala  
 100 105 110

gtc ccc act tcc gaa ctt ccg gct cac ttc ctt tcc cac tgc gag cgc 384  
 Val Pro Thr Ser Glu Leu Pro Ala His Phe Leu Ser His Cys Glu Arg  
 115 120 125

att aaa gcc acc aac ggc aaa gat cgg gtg atc atg cac tgc cac gcc 432  
 Ile Lys Ala Thr Asn Gly Lys Asp Arg Val Ile Met His Cys His Ala  
 130 135 140

acc aac ctg atc gcc ctc acc tat gta ctt gaa aac gac acc gcg gtc 480  
 Thr Asn Leu Ile Ala Leu Thr Tyr Val Leu Glu Asn Asp Thr Ala Val  
 145 150 155 160

ttc act cgc caa ctg tgg gaa ggc agc acc gag tgt ctg gtg gta ttc 528  
 Phe Thr Arg Gln Leu Trp Glu Gly Ser Thr Glu Cys Leu Val Val Phe  
 165 170 175

ccg gat ggc gtt ggc att ttg ccg tgg atg gtg ccc ggc acg gac gaa 576  
 Pro Asp Gly Val Gly Ile Leu Pro Trp Met Val Pro Gly Thr Asp Glu  
 180 185 190

atc ggc cag gcg acc gca caa gag atg caa aaa cat tcg ctg gtg ttg 624  
 Ile Gly Gln Ala Thr Ala Gln Glu Met Gln Lys His Ser Leu Val Leu  
 195 200 205

tgg ccc ttc cac ggc gtc ttc ggc agc gga ccg acg ctg gat gaa acc 672  
 Trp Pro Phe His Gly Val Phe Gly Ser Gly Pro Thr Leu Asp Glu Thr  
 210 215 220

ttc ggt tta atc gac acc gca gaa aaa tca gca caa gta tta gtg aag 720  
 Phe Gly Leu Ile Asp Thr Ala Glu Lys Ser Ala Gln Val Leu Val Lys  
 225 230 235 240

gtt tat tcg atg ggc ggc atg aaa cag acc atc agc cgt gaa gag ttg 768  
 Val Tyr Ser Met Gly Gly Met Lys Gln Thr Ile Ser Arg Glu Glu Leu  
 245 250 255

ata gcg ctc ggc aag cgt ttc ggc gtt acg cca ctc gcc agt gcg ctg 816  
 Ile Ala Leu Gly Lys Arg Phe Gly Val Thr Pro Leu Ala Ser Ala Leu  
 260 265 270

gcg ctg taa 825  
 Ala Leu

<210> 13  
 <211> 274  
 <212> PRT  
 <213> Escherichia coli

<400> 13  
 Met Gln Asn Ile Thr Gln Ser Trp Phe Val Gln Gly Met Ile Lys Ala  
 1 5 10 15  
 Thr Thr Asp Ala Trp Leu Lys Gly Trp Asp Glu Arg Asn Gly Gly Asn  
 20 25 30  
 Leu Thr Leu Arg Leu Asp Asp Ala Asp Ile Ala Pro Tyr His Asp Asn  
 35 40 45  
 Phe His Gln Gln Pro Arg Tyr Ile Pro Leu Ser Gln Pro Met Pro Leu  
 50 55 60  
 Leu Ala Asn Thr Pro Phe Ile Val Thr Gly Ser Gly Lys Phe Phe Arg  
 65 70 75 80

[illegible]

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<210> 14
<211> 939
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(936)
<223> coding for rhaR (positive regulator for rhaRS
operon)
```

<400> 14																	
atg	gct	ttc	tgc	aat	aac	gcg	aat	ctt	ctc	aac	gta	ttt	gta	cgc	cat	48	
Met	Ala	Phe	Cys	Asn	Asn	Ala	Asn	Leu	Leu	Asn	Val	Phe	Val	Arg	His		
1				5					10					15			
att	gcg	aat	aat	caa	ctt	cgt	tct	ctg	gcc	gag	gta	gcc	acg	gtg	gcg	96	
Ile	Ala	Asn	Asn	Gln	Leu	Arg	Ser	Leu	Ala	Glu	Val	Ala	Thr	Val	Ala		
				20				25					30				
cat	cag	tta	aaa	ctt	ctc	aaa	gat	gat	ttt	ttt	gcc	agc	gac	cag	cag	144	
His	Gln	Leu	Lys	Leu	Leu	Lys	Asp	Asp	Phe	Phe	Ala	Ser	Asp	Gln	Gln		
		35					40					45					
gca	gtc	gct	gtg	gct	gac	cgt	tat	ccg	caa	gat	gtc	ttt	gct	gaa	cat	192	
Ala	Val	Ala	Val	Ala	Asp	Arg	Tyr	Pro	Gln	Asp	Val	Phe	Ala	Glu	His		
50						55					60						

## 15

aca	cat	gat	ttt	tgt	gag	ctg	gtg	att	gtc	tgg	cgc	ggt	aat	ggc	ctg	240
Thr	His	Asp	Phe	Cys	Glu	Leu	Val	Ile	Val	Trp	Arg	Gly	Asn	Gly	Leu	
65					70					75					80	
cat	gta	ctc	aac	gat	cgc	cct	tat	cgc	att	acc	cgt	ggc	gat	ctc	ttt	288
His	Val	Leu	Asn	Asp	Arg	Pro	Tyr	Arg	Ile	Thr	Arg	Gly	Asp	Leu	Phe	
				85					90					95		
tac	att	cat	gct	gac	gat	aaa	cac	tcc	tac	gct	tcc	gtt	aac	gat	ctg	336
Tyr	Ile	His	Ala	Asp	Asp	Lys	His	Ser	Tyr	Ala	Ser	Val	Asn	Asp	Leu	
			100					105					110			
gtt	ttg	cag	aat	att	att	tat	tgc	ccg	gag	cgt	ctg	aag	ctg	aat	ctt	384
Val	Leu	Gln	Asn	Ile	Ile	Tyr	Cys	Pro	Glu	Arg	Leu	Lys	Leu	Asn	Leu	
		115					120					125				
gac	tgg	cag	ggg	gcg	att	ccg	gga	ttt	aac	gcc	agc	gca	ggg	caa	cca	432
Asp	Trp	Gln	Gly	Ala	Ile	Pro	Gly	Phe	Asn	Ala	Ser	Ala	Gly	Gln	Pro	
	130					135					140					
cac	tgg	cgc	tta	ggt	agc	atg	ggg	atg	gcg	cag	gcg	cgg	cag	gtt	atc	480
His	Trp	Arg	Leu	Gly	Ser	Met	Gly	Met	Ala	Gln	Ala	Arg	Gln	Val	Ile	
145					150				155						160	
ggt	cag	ctt	gag	cat	gaa	agt	agt	cag	cat	gtg	ccg	ttt	gct	aac	gaa	528
Gly	Gln	Leu	Glu	His	Glu	Ser	Ser	Gln	His	Val	Pro	Phe	Ala	Asn	Glu	
				165					170					175		
atg	gct	gag	ttg	ctg	ttc	ggg	cag	ttg	gtg	atg	ttg	ctg	aat	cgc	cat	576
Met	Ala	Glu	Leu	Leu	Phe	Gly	Gln	Leu	Val	Met	Leu	Leu	Asn	Arg	His	
			180					185					190			
cgt	tac	acc	agt	gat	tcg	ttg	ccg	cca	aca	tcc	agc	gaa	acg	ttg	ctg	624
Arg	Tyr	Thr	Ser	Asp	Ser	Leu	Pro	Pro	Thr	Ser	Ser	Glu	Thr	Leu	Leu	
		195					200					205				
gat	aag	ctg	att	acc	cgg	ctg	gcg	gct	agc	ctg	aaa	agt	ccc	ttt	gcg	672
Asp	Lys	Leu	Ile	Thr	Arg	Leu	Ala	Ala	Ser	Leu	Lys	Ser	Pro	Phe	Ala	
	210					215					220					
ctg	gat	aaa	ttt	tgt	gat	gag	gca	tcg	tgc	agt	gag	cgc	gtt	ttg	cgt	720
Leu	Asp	Lys	Phe	Cys	Asp	Glu	Ala	Ser	Cys	Ser	Glu	Arg	Val	Leu	Arg	
225					230					235					240	
cag	caa	ttt	cgc	cag	cag	act	gga	atg	acc	atc	aat	caa	tat	ctg	cga	768
Gln	Gln	Phe	Arg	Gln	Gln	Thr	Gly	Met	Thr	Ile	Asn	Gln	Tyr	Leu	Arg	
				245					250					255		
cag	gtc	aga	gtg	tgt	cat	gcg	caa	tat	ctt	ctc	cag	cat	agc	cgc	ctg	816
Gln	Val	Arg	Val	Cys	His	Ala	Gln	Tyr	Leu	Leu	Gln	His	Ser	Arg	Leu	
			260					265					270			
tta	atc	agt	gat	att	tcg	acc	gaa	tgt	ggc	ttt	gaa	gat	agt	aac	tat	864
Leu	Ile	Ser	Asp	Ile	Ser	Thr	Glu	Cys	Gly	Phe	Glu	Asp	Ser	Asn	Tyr	
		275					280					285				
ttt	tcg	gtg	gtg	ttt	acc	cgg	gaa	acc	ggg	atg	acg	ccc	agc	cag	tgg	912
Phe	Ser	Val	Val	Phe	Thr	Arg	Glu	Thr	Gly	Met	Thr	Pro	Ser	Gln	Trp	
	290					295					300					
cgt	cat	ctc	aat	tcg	cag	aaa	gat	taa								939
Arg	His	Leu	Asn	Ser	Gln	Lys	Asp									
305					310											

&lt;210&gt; 15

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 15

```

Met Ala Phe Cys Asn Asn Ala Asn Leu Leu Asn Val Phe Val Arg His
 1           5           10           15
Ile Ala Asn Asn Gln Leu Arg Ser Leu Ala Glu Val Ala Thr Val Ala
          20           25           30
His Gln Leu Lys Leu Leu Lys Asp Asp Phe Phe Ala Ser Asp Gln Gln
          35           40           45
Ala Val Ala Val Ala Asp Arg Tyr Pro Gln Asp Val Phe Ala Glu His
          50           55           60
Thr His Asp Phe Cys Glu Leu Val Ile Val Trp Arg Gly Asn Gly Leu
 65           70           75           80
His Val Leu Asn Asp Arg Pro Tyr Arg Ile Thr Arg Gly Asp Leu Phe
          85           90           95
Tyr Ile His Ala Asp Asp Lys His Ser Tyr Ala Ser Val Asn Asp Leu
          100          105          110
Val Leu Gln Asn Ile Ile Tyr Cys Pro Glu Arg Leu Lys Leu Asn Leu
          115          120          125
Asp Trp Gln Gly Ala Ile Pro Gly Phe Asn Ala Ser Ala Gly Gln Pro
          130          135          140
His Trp Arg Leu Gly Ser Met Gly Met Ala Gln Ala Arg Gln Val Ile
          145          150          155          160
Gly Gln Leu Glu His Glu Ser Ser Gln His Val Pro Phe Ala Asn Glu
          165          170          175
Met Ala Glu Leu Leu Phe Gly Gln Leu Val Met Leu Leu Asn Arg His
          180          185          190
Arg Tyr Thr Ser Asp Ser Leu Pro Pro Thr Ser Ser Glu Thr Leu Leu
          195          200          205
Asp Lys Leu Ile Thr Arg Leu Ala Ala Ser Leu Lys Ser Pro Phe Ala
          210          215          220
Leu Asp Lys Phe Cys Asp Glu Ala Ser Cys Ser Glu Arg Val Leu Arg
          225          230          235          240
Gln Gln Phe Arg Gln Gln Thr Gly Met Thr Ile Asn Gln Tyr Leu Arg
          245          250          255
Gln Val Arg Val Cys His Ala Gln Tyr Leu Leu Gln His Ser Arg Leu
          260          265          270
Leu Ile Ser Asp Ile Ser Thr Glu Cys Gly Phe Glu Asp Ser Asn Tyr
          275          280          285
Phe Ser Val Val Phe Thr Arg Glu Thr Gly Met Thr Pro Ser Gln Trp
          290          295          300
Arg His Leu Asn Ser Gln Lys Asp
          305          310

```

&lt;210&gt; 16

&lt;211&gt; 837

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(834)

&lt;223&gt; coding for rhaS (positive regulator of rhaBAD operon)

&lt;400&gt; 16

atg acc gta tta cat agt gtg gat ttt ttt ccg tct ggt aac gcg tcc	48
Met Thr Val Leu His Ser Val Asp Phe Phe Pro Ser Gly Asn Ala Ser	
1 5 10 15	
gtg gcg ata gaa ccc cgg ctc ccg cag gcg gat ttt cct gaa cat cat	96
Val Ala Ile Glu Pro Arg Leu Pro Gln Ala Asp Phe Pro Glu His His	
20 25 30	
cat gat ttt cat gaa att gtg att gtc gaa cat ggc acg ggt att cat	144
His Asp Phe His Glu Ile Val Ile Val Glu His Gly Thr Gly Ile His	
35 40 45	
gtg ttt aat ggg cag ccc tat acc atc acc ggt ggc acg gtc tgt ttc	192
Val Phe Asn Gly Gln Pro Tyr Thr Ile Thr Gly Gly Thr Val Cys Phe	
50 55 60	
gta cgc gat cat gat cgg cat ctg tat gaa cat acc gat aat ctg tgt	240
Val Arg Asp His Asp Arg His Leu Tyr Glu His Thr Asp Asn Leu Cys	
65 70 75 80	
ctg acc aat gtg ctg tat cgc tcg ccg gat cga ttt cag ttt ctc gcc	288
Leu Thr Asn Val Leu Tyr Arg Ser Pro Asp Arg Phe Gln Phe Leu Ala	
85 90 95	
ggg ctg aat cag ttg ctg cca caa gag ctg gat ggg cag tat ccg tct	336
Gly Leu Asn Gln Leu Leu Pro Gln Glu Leu Asp Gly Gln Tyr Pro Ser	
100 105 110	
cac tgg cgc gtt aac cac agc gta ttg cag cag gtg cga cag ctg gtt	384
His Trp Arg Val Asn His Ser Val Leu Gln Gln Val Arg Gln Leu Val	
115 120 125	
gca cag atg gaa cag cag gaa ggg gaa aat gat tta ccc tcg acc gcc	432
Ala Gln Met Glu Gln Gln Glu Gly Glu Asn Asp Leu Pro Ser Thr Ala	
130 135 140	
agt cgc gag atc ttg ttt atg caa tta ctg ctc ttg ctg cgt aaa agc	480
Ser Arg Glu Ile Leu Phe Met Gln Leu Leu Leu Leu Leu Arg Lys Ser	
145 150 155 160	
agt ttg cag gag aac ctg gaa aac agc gca tca cgt ctc aac ttg ctt	528
Ser Leu Gln Glu Asn Leu Glu Asn Ser Ala Ser Arg Leu Asn Leu Leu	
165 170 175	
ctg gcc tgg ctg gag gac cat ttt gcc gat gag gtg aat tgg gat gcc	576
Leu Ala Trp Leu Glu Asp His Phe Ala Asp Glu Val Asn Trp Asp Ala	
180 185 190	
gtg gcg gat caa ttt tct ctt tca ctg cgt acg cta cat cgg cag ctt	624
Val Ala Asp Gln Phe Ser Leu Ser Leu Arg Thr Leu His Arg Gln Leu	
195 200 205	
aag cag caa acg gga ctg acg cct cag cga tac ctg aac cgc ctg cga	672
Lys Gln Gln Thr Gly Leu Thr Pro Gln Arg Tyr Leu Asn Arg Leu Arg	
210 215 220	
ctg atg aaa gcc cga cat ctg cta cgc cac agc gag gcc agc gtt act	720
Leu Met Lys Ala Arg His Leu Leu Arg His Ser Glu Ala Ser Val Thr	
225 230 235 240	

## 18

gac atc gcc tat cgc tgt gga ttc agc gac agt aac cac ttt tcg acg 768  
 Asp Ile Ala Tyr Arg Cys Gly Phe Ser Asp Ser Asn His Phe Ser Thr  
                   245                                  250                                  255

ctt ttt cgc cga gag ttt aac tgg tca ccg cgt gat att cgc cag gga 816  
 Leu Phe Arg Arg Glu Phe Asn Trp Ser Pro Arg Asp Ile Arg Gln Gly  
                   260                                  265                                  270

cgg gat ggc ttt ctg caa taa 837  
 Arg Asp Gly Phe Leu Gln  
                   275

<210> 17

<211> 278

<212> PRT

<213> Escherichia coli

<400> 17

Met Thr Val Leu His Ser Val Asp Phe Phe Pro Ser Gly Asn Ala Ser  
   1                                  5                                  10                                  15

Val Ala Ile Glu Pro Arg Leu Pro Gln Ala Asp Phe Pro Glu His His  
                   20                                  25                                  30

His Asp Phe His Glu Ile Val Ile Val Glu His Gly Thr Gly Ile His  
                   35                                  40                                  45

Val Phe Asn Gly Gln Pro Tyr Thr Ile Thr Gly Gly Thr Val Cys Phe  
                   50                                  55                                  60

Val Arg Asp His Asp Arg His Leu Tyr Glu His Thr Asp Asn Leu Cys  
   65                                  70                                  75                                  80

Leu Thr Asn Val Leu Tyr Arg Ser Pro Asp Arg Phe Gln Phe Leu Ala  
                   85                                  90                                  95

Gly Leu Asn Gln Leu Leu Pro Gln Glu Leu Asp Gly Gln Tyr Pro Ser  
                   100                                  105                                  110

His Trp Arg Val Asn His Ser Val Leu Gln Gln Val Arg Gln Leu Val  
                   115                                  120                                  125

Ala Gln Met Glu Gln Gln Glu Gly Glu Asn Asp Leu Pro Ser Thr Ala  
                   130                                  135                                  140

Ser Arg Glu Ile Leu Phe Met Gln Leu Leu Leu Leu Leu Arg Lys Ser  
  145                                  150                                  155                                  160

Ser Leu Gln Glu Asn Leu Glu Asn Ser Ala Ser Arg Leu Asn Leu Leu  
                   165                                  170                                  175

Leu Ala Trp Leu Glu Asp His Phe Ala Asp Glu Val Asn Trp Asp Ala  
                   180                                  185                                  190

Val Ala Asp Gln Phe Ser Leu Ser Leu Arg Thr Leu His Arg Gln Leu  
                   195                                  200                                  205

Lys Gln Gln Thr Gly Leu Thr Pro Gln Arg Tyr Leu Asn Arg Leu Arg  
  210                                  215                                  220

Leu Met Lys Ala Arg His Leu Leu Arg His Ser Glu Ala Ser Val Thr  
  225                                  230                                  235                                  240

Asp Ile Ala Tyr Arg Cys Gly Phe Ser Asp Ser Asn His Phe Ser Thr  
                   245                                  250                                  255

Leu Phe Arg Arg Glu Phe Asn Trp Ser Pro Arg Asp Ile Arg Gln Gly  
                   260                                  265                                  270

Arg Asp Gly Phe Leu Gln  
275

<210> 18

<211> 1035

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(1032)

<223> coding for rhaT (rhamnose transport protein)

<400> 18

atg agt aac gcg att acg atg ggg ata ttt tgg cat ttg atc ggc gcg	48
Met Ser Asn Ala Ile Thr Met Gly Ile Phe Trp His Leu Ile Gly Ala	
1 5 10 15	
gcc agt gca gcc tgt ttt tac gct ccg ttc aaa aaa gta aaa aaa tgg	96
Ala Ser Ala Ala Cys Phe Tyr Ala Pro Phe Lys Lys Val Lys Lys Trp	
20 25 30	
tca tgg gaa acc atg tgg tca gtc ggt ggg att gtt tcg tgg att att	144
Ser Trp Glu Thr Met Trp Ser Val Gly Gly Ile Val Ser Trp Ile Ile	
35 40 45	
ctg ccg tgg gcc atc agc gcc ctg tta cta ccg aat ttc tgg gcg tat	192
Leu Pro Trp Ala Ile Ser Ala Leu Leu Leu Pro Asn Phe Trp Ala Tyr	
50 55 60	
tac agc tcg ttt agt ctc tct acg cga ctg cct gtt ttt ctg ttc ggc	240
Tyr Ser Ser Phe Ser Leu Ser Thr Arg Leu Pro Val Phe Leu Phe Gly	
65 70 75 80	
gct atg tgg ggg atc ggt aat atc aac tac ggc ctg acc atg cgt tat	288
Ala Met Trp Gly Ile Gly Asn Ile Asn Tyr Gly Leu Thr Met Arg Tyr	
85 90 95	
ctc ggc atg tcg atg gga att ggc atc gcc att ggc att acg ttg att	336
Leu Gly Met Ser Met Gly Ile Gly Ile Ala Ile Gly Ile Thr Leu Ile	
100 105 110	
gtc ggt acg ctg atg acg cca att atc aac ggc aat ttc gat gtg ttg	384
Val Gly Thr Leu Met Thr Pro Ile Ile Asn Gly Asn Phe Asp Val Leu	
115 120 125	
att agc acc gaa ggc gga cgc atg acg ttg ctc ggc gtt ctg gtg gcg	432
Ile Ser Thr Glu Gly Gly Arg Met Thr Leu Leu Gly Val Leu Val Ala	
130 135 140	
ctg att ggc gta ggg att gta act cgc gcc ggg cag ttg aaa gag cgc	480
Leu Ile Gly Val Gly Ile Val Thr Arg Ala Gly Gln Leu Lys Glu Arg	
145 150 155 160	
aag atg ggc att aaa gcc gaa gag ttc aat ctg aaa aaa ggg ctg gtg	528
Lys Met Gly Ile Lys Ala Glu Glu Phe Asn Leu Lys Lys Gly Leu Val	
165 170 175	
ctg gcg gtg atg tgc ggc att ttc tct gcc ggg atg tcc ttt gcg atg	576
Leu Ala Val Met Cys Gly Ile Phe Ser Ala Gly Met Ser Phe Ala Met	
180 185 190	
aac gcc gca aaa ccg atg cat gaa gcc gct gcc gca ctt ggc gtc gat	624
Asn Ala Ala Lys Pro Met His Glu Ala Ala Ala Ala Leu Gly Val Asp	
195 200 205	

## 20

cca	ctg	tat	gtc	gct	ctg	cca	agc	tat	gtt	gtc	atc	atg	ggc	ggc	ggc	672
Pro	Leu	Tyr	Val	Ala	Leu	Pro	Ser	Tyr	Val	Val	Ile	Met	Gly	Gly	Gly	
210						215					220					
gcg	atc	att	aac	ctc	ggt	ttc	tgt	ttt	att	cgt	ctg	gca	aaa	gtg	aag	720
Ala	Ile	Ile	Asn	Leu	Gly	Phe	Cys	Phe	Ile	Arg	Leu	Ala	Lys	Val	Lys	
225					230					235					240	
gat	ttg	tcg	cta	aaa	gcc	gac	ttc	tcg	ctg	gca	aaa	tcg	ctg	atc	att	768
Asp	Leu	Ser	Leu	Lys	Ala	Asp	Phe	Ser	Leu	Ala	Lys	Ser	Leu	Ile	Ile	
				245					250					255		
cac	aat	gtg	tta	ctc	tcg	aca	ctg	ggc	ggg	ttg	atg	tgg	tat	ctg	caa	816
His	Asn	Val	Leu	Leu	Ser	Thr	Leu	Gly	Gly	Leu	Met	Trp	Tyr	Leu	Gln	
			260					265					270			
ttc	ttt	ttc	tat	gcc	tgg	ggc	cac	gcc	cgc	att	ccg	gcg	cag	tat	gac	864
Phe	Phe	Phe	Tyr	Ala	Trp	Gly	His	Ala	Arg	Ile	Pro	Ala	Gln	Tyr	Asp	
		275					280					285				
tac	atc	agt	tgg	atg	ctg	cat	atg	agt	ttc	tat	gta	ttg	tgc	ggc	ggt	912
Tyr	Ile	Ser	Trp	Met	Leu	His	Met	Ser	Phe	Tyr	Val	Leu	Cys	Gly	Gly	
	290					295					300					
atc	gtc	ggg	ctg	gtg	ctg	aaa	gag	tgg	aac	aat	gca	gga	cgc	cgt	ccg	960
Ile	Val	Gly	Leu	Val	Leu	Lys	Glu	Trp	Asn	Asn	Ala	Gly	Arg	Arg	Pro	
305					310					315					320	
gta	acg	gtg	ttg	agc	ctc	ggt	tgt	gtg	gtg	att	att	gtc	gcc	gct	aac	1008
Val	Thr	Val	Leu	Ser	Leu	Gly	Cys	Val	Val	Ile	Ile	Val	Ala	Ala	Asn	
				325				330						335		
atc	gtc	ggc	atc	ggc	atg	gcg	aat	taa								1035
Ile	Val	Gly	Ile	Gly	Met	Ala	Asn									
			340													

&lt;210&gt; 19

&lt;211&gt; 344

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 19

Met	Ser	Asn	Ala	Ile	Thr	Met	Gly	Ile	Phe	Trp	His	Leu	Ile	Gly	Ala	
1				5					10					15		
Ala	Ser	Ala	Ala	Cys	Phe	Tyr	Ala	Pro	Phe	Lys	Lys	Val	Lys	Lys	Trp	
		20						25					30			
Ser	Trp	Glu	Thr	Met	Trp	Ser	Val	Gly	Gly	Ile	Val	Ser	Trp	Ile	Ile	
		35					40					45				
Leu	Pro	Trp	Ala	Ile	Ser	Ala	Leu	Leu	Leu	Pro	Asn	Phe	Trp	Ala	Tyr	
	50					55					60					
Tyr	Ser	Ser	Phe	Ser	Leu	Ser	Thr	Arg	Leu	Pro	Val	Phe	Leu	Phe	Gly	
	65				70				75						80	
Ala	Met	Trp	Gly	Ile	Gly	Asn	Ile	Asn	Tyr	Gly	Leu	Thr	Met	Arg	Tyr	
				85				90						95		
Leu	Gly	Met	Ser	Met	Gly	Ile	Gly	Ile	Ala	Ile	Gly	Ile	Thr	Leu	Ile	
			100					105					110			
Val	Gly	Thr	Leu	Met	Thr	Pro	Ile	Ile	Asn	Gly	Asn	Phe	Asp	Val	Leu	
	115						120					125				
Ile	Ser	Thr	Glu	Gly	Gly	Arg	Met	Thr	Leu	Leu	Gly	Val	Leu	Val	Ala	
	130					135					140					

## 21

Leu	Ile	Gly	Val	Gly	Ile	Val	Thr	Arg	Ala	Gly	Gln	Leu	Lys	Glu	Arg	145	150	155	160
Lys	Met	Gly	Ile	Lys	Ala	Glu	Glu	Phe	Asn	Leu	Lys	Lys	Gly	Leu	Val	165	170		175
Leu	Ala	Val	Met	Cys	Gly	Ile	Phe	Ser	Ala	Gly	Met	Ser	Phe	Ala	Met	180	185		190
Asn	Ala	Ala	Lys	Pro	Met	His	Glu	Ala	Ala	Ala	Ala	Leu	Gly	Val	Asp	195	200		205
Pro	Leu	Tyr	Val	Ala	Leu	Pro	Ser	Tyr	Val	Val	Ile	Met	Gly	Gly	Gly	210	215		220
Ala	Ile	Ile	Asn	Leu	Gly	Phe	Cys	Phe	Ile	Arg	Leu	Ala	Lys	Val	Lys	225	230		235
Asp	Leu	Ser	Leu	Lys	Ala	Asp	Phe	Ser	Leu	Ala	Lys	Ser	Leu	Ile	Ile	245	250		255
His	Asn	Val	Leu	Leu	Ser	Thr	Leu	Gly	Gly	Leu	Met	Trp	Tyr	Leu	Gln	260	265		270
Phe	Phe	Phe	Tyr	Ala	Trp	Gly	His	Ala	Arg	Ile	Pro	Ala	Gln	Tyr	Asp	275	280		285
Tyr	Ile	Ser	Trp	Met	Leu	His	Met	Ser	Phe	Tyr	Val	Leu	Cys	Gly	Gly	290	295		300
Ile	Val	Gly	Leu	Val	Leu	Lys	Glu	Trp	Asn	Asn	Ala	Gly	Arg	Arg	Pro	305	310		315
Val	Thr	Val	Leu	Ser	Leu	Gly	Cys	Val	Val	Ile	Ile	Val	Ala	Ala	Asn	325	330		335
Ile	Val	Gly	Ile	Gly	Met	Ala	Asn									340			

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